

Refine Search

Search Results -

Terms	Documents
L2 and gpcr	4

Database:

US Pre-Grant Publication Full-Text Database
 US Patents Full-Text Database
 US OCR Full-Text Database
 EPO Abstracts Database
 JPO Abstracts Database
 Derwent World Patents Index
 IBM Technical Disclosure Bulletins

Search:

L3



Refine Search

Recall Text

Clear

Interrupt

Search History

DATE: Wednesday, August 30, 2006 [Purge Queries](#) [Printable Copy](#) [Create Case](#)

Set Name **Query**
 side by side

Hit Count **Set Name**
 result set

DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI,TDBD; PLUR=YES; OP=ADJ

<u>L3</u>	L2 and gpcr	4	<u>L3</u>
<u>L2</u>	hrup35 or gpr139 or pgr3 or gprg1 or rup35	48	<u>L2</u>
<u>L1</u>	hrup35 or gpr139 or pgr3 or gprg1	17	<u>L1</u>

END OF SEARCH HISTORY

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b-15.rge.

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:30:29 ; Search time 7935.45 Seconds
 (without alignments)
 8558.076 Million cell updates/sec

Title: US-09-995-225B-15
 Perfect score: 1062
 Sequence: 1 atggagcacacgcacgcca.....ctataaaagtatccccgtga 1062

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : GenEmbl:*
 1: gb_env:*
 2: gb_pat:*
 3: gb_ph:*
 4: gb_pl:*
 5: gb_pr:*
 6: gb_ro:*
 7: gb_sts:*
 8: gb_sy:*
 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1062	100.0	1062	2	BD103852	BD103852 Novel G p
2	1062	100.0	1062	2	BD183204	BD183204 Novel G p
3	1062	100.0	1062	2	AX498192	AX498192 Sequence
4	1062	100.0	2117	2	CQ867782	CQ867782 Sequence
5	1061.6	100.0	1167	5	AY635179	AY635179 Homo sapi
6	1060.4	99.8	1062	2	BD103851	BD103851 Novel G p
7	1060.4	99.8	1062	2	BD183203	BD183203 Novel G p
8	1060.4	99.8	1062	5	AB196529	AB196529 Homo sapi
9	1058.8	99.7	1343	2	AX254977	AX254977 Sequence
10	1057.4	99.6	1059	2	AX463227	AX463227 Sequence
11	1050.8	98.9	1062	2	AX664703	AX664703 Sequence
12	1050.8	98.9	1526	2	AX664701	AX664701 Sequence
13	1048.4	98.7	1119	2	AX254975	AX254975 Sequence
14	1048.4	98.7	1130	2	AX375235	AX375235 Sequence
15	945.2	89.0	1062	2	AX463235	AX463235 Sequence
16	940.2	88.5	957	2	CQ737667	CQ737667 Sequence
c 17	938	88.3	110000	12	AL139235_0	AL139235 Homo sapi
18	936.4	88.2	1002	2	AX375442	AX375442 Sequence
19	936.4	88.2	1158	2	BD144286	BD144286 Novel G-p
20	936.4	88.2	1167	2	CQ848070	CQ848070 Sequence
21	936.4	88.2	1167	5	AB083594	AB083594 Homo sapi
c 22	936.4	88.2	101882	5	AC021089	AC021089 Homo sapi
23	936	88.1	1032	2	AX463231	AX463231 Sequence
24	936	88.1	1070	2	AX463230	AX463230 Sequence
25	936	88.1	1826	2	AX463232	AX463232 Sequence
26	934.8	88.0	1000	2	AX342465	AX342465 Sequence
27	934.8	88.0	1788	2	CQ739127	CQ739127 Sequence
28	844	79.5	1038	6	AB196532	AB196532 Mus muscu
c 29	842.6	79.3	864	2	AX230119	AX230119 Sequence
30	842.4	79.3	1038	6	AY485344	AY485344 Mus muscu
31	834.4	78.6	1038	6	AB196531	AB196531 Rattus no
c 32	821.2	77.3	196833	12	AC164864	AC164864 Bos tauru
33	809.6	76.2	963	2	AX657444	AX657444 Sequence
34	788.4	74.2	183326	6	AC124438	AC124438 Mus muscu
c 35	779.6	73.4	140885	12	AC119798	AC119798 Rattus no
c 36	779.6	73.4	203372	12	AC121346	AC121346 Rattus no
c 37	779.6	73.4	230813	12	AC114097	AC114097 Rattus no
38	758	71.4	795	2	AX549301	AX549301 Sequence
39	758	71.4	795	5	HSA303165	AJ303165 Homo sapi
40	666.2	62.7	823	7	BV677579	BV677579 GPR139_7
41	555.4	52.3	558	5	AY255545	AY255545 Homo sapi
c 42	524	49.3	930	2	AX230116	AX230116 Sequence
43	444.4	41.8	1149	11	AY288414	AY288414 Takifugu
44	412.6	38.9	242078	11	CR846080	CR846080 Zebrafish
45	268.2	25.3	945	5	AY255622	AY255622 Homo sapi

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b-15.rng.

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OM nucleic - nucleic search, using sw model

```
Run on:      August 24, 2006, 16:24:07 ; Search time 1137.31 Seconds
              (without alignments)
              6510.549 Million cell updates/sec
```

Title: US-09-995-225B-15
Perfect score: 1062
Sequence: 1 atggagcacacgcacgcca.....ctataaaagtatccccqtga 1062

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1062	100.0	1062	6	ABK15563	Abk15563 cDNA enco
2	1062	100.0	1062	6	ABT04873	Abt04873 Human G p
3	1062	100.0	1062	10	ACC44115	Acc44115 Human AXO
4	1062	100.0	2117	13	ADR16433	Adr16433 Human KOR
5	1060.4	99.8	1062	6	ABK15562	Abk15562 cDNA enco
6	1060.4	99.8	1062	10	ACC71785	Acc71785 Human G p
7	1060.4	99.8	1202	8	ABV73364	Abv73364 Human TGR
8	1060	99.8	1776	10	ADF70587	Adf70587 Orphan re
9	1058.8	99.7	1343	4	AAS15731	Aas15731 DNA encod
10	1058.8	99.7	1343	10	ADJ87768	Adj87768 G-coupled
11	1058.8	99.7	1343	12	ADI79324	Adi79324 NOV11 cod
12	1058.8	99.7	1343	12	ADO56003	Ado56003 DNA encod
13	1058.8	99.7	2273	12	ADO28955	Ado28955 Human nov
14	1057.4	99.6	1059	6	ABN84269	Abn84269 Human che
15	1050.8	98.9	1526	6	AAD46858	Aad46858 Human 7TM
16	1050.8	98.9	1526	8	ACA60889	Aca60889 Human cDN
17	1050.8	98.9	1526	10	ABS57024	Abs57024 cDNA enco
18	1048.4	98.7	1119	4	AAS15730	Aas15730 DNA encod
19	1048.4	98.7	1119	10	ADJ87766	Adj87766 G-coupled
20	1048.4	98.7	1119	12	ADI79322	Adi79322 NOV10a co
21	1048.4	98.7	1119	12	ADO56001	Ado56001 DNA encod
22	1048.4	98.7	1130	6	AAD29672	Aad29672 Human G-p
23	1048.4	98.7	2198	9	ACF05275	Acf05275 Human G-p
24	1039.8	97.9	1110	9	ACF05276	Acf05276 Human G-p
25	1039.8	97.9	2189	10	ADD18120	Add18120 Human G-p
26	945.2	89.0	1062	6	ABN84273	Abn84273 Human che
27	940.2	88.5	957	12	ADI79347	Adi79347 NOV10b co
28	940.2	88.5	957	12	ADO56026	Ado56026 DNA encod
29	936.4	88.2	1002	6	AAD27501	Aad27501 Human G-p
30	936.4	88.2	1002	10	AAD61658	Aad61658 Human GPC
31	936.4	88.2	1158	6	ABZ42880	Abz42880 Human GPC
32	936.4	88.2	1167	13	ADQ89945	Adq89945 Antagonis
33	936	88.1	1032	6	ABN84271	Abn84271 Human che
34	936	88.1	1070	6	ABN84270	Abn84270 Human che
35	936	88.1	1826	6	ABN84272	Abn84272 Human che
36	934.8	88.0	1000	6	AAD28102	Aad28102 Human thy
37	917.2	86.4	946	10	ADJ87879	Adj87879 G-coupled
38	844	79.5	1038	8	ABV73373	Abv73373 Mouse TGR
39	844	79.5	1038	12	ADO28957	Ado28957 Mouse nov
c 40	842.6	79.3	864	4	AAS42811	Aas42811 Human G P
41	828.4	78.0	867	6	AAS98134	Aas98134 Human DNA
c 42	828.4	78.0	894	6	AAS98143	Aas98143 Human DNA
43	809.6	76.2	963	10	ADC12695	Adc12695 Human GPC
44	758	71.4	795	6	AAS98071	Aas98071 Human DNA
45	758	71.4	795	8	ABZ42552	Abz42552 Human G p

ALIGNMENTS

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b- 15.rni.

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:44:27 ; Search time 362.262 Seconds
(without alignments)
5485.303 Million cell updates/sec

Title: US-09-995-225B-15
Perfect score: 1062
Sequence: 1 atggagcacacgcacgcca.....ctataaaagtatccccgtga 1062

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	63.2	6.0	10304	3	US-09-627-465B-1	Sequence 1, Appli
	2	59.6	5.6	7218	2	US-08-232-463-14	Sequence 14, Appl
c	3	57.8	5.4	31391	3	US-09-949-016-14319	Sequence 14319, A
c	4	52.6	5.0	134008	3	US-09-949-016-13841	Sequence 13841, A
c	5	51.8	4.9	767677	3	US-09-949-016-12147	Sequence 12147, A
c	6	51.8	4.9	767677	3	US-09-949-016-17361	Sequence 17361, A
c	7	50.8	4.8	39154	3	US-09-949-016-12384	Sequence 12384, A
c	8	50.8	4.8	39154	3	US-09-949-016-12801	Sequence 12801, A
c	9	50.8	4.8	39443	3	US-09-949-016-14326	Sequence 14326, A
c	10	50.8	4.8	39443	3	US-09-949-016-14327	Sequence 14327, A
c	11	48.2	4.5	522	3	US-09-949-016-103758	Sequence 103758,
c	12	47	4.4	30656	3	US-09-949-016-14613	Sequence 14613, A
c	13	47	4.4	142783	3	US-09-949-016-15127	Sequence 15127, A
c	14	46.8	4.4	2518	3	US-09-433-699-3	Sequence 3, Appli
c	15	46.8	4.4	2527	3	US-09-949-016-4169	Sequence 4169, Ap
	16	46.2	4.4	951	2	US-08-671-525B-1	Sequence 1, Appli
	17	46.2	4.4	951	2	US-08-672-109B-1	Sequence 1, Appli
	18	46.2	4.4	951	2	US-08-842-045-1	Sequence 1, Appli
	19	46.2	4.4	951	2	US-08-842-238-1	Sequence 1, Appli
	20	46.2	4.4	951	3	US-08-629-335B-1	Sequence 1, Appli
	21	46.2	4.4	1149	3	US-09-868-552-1	Sequence 1, Appli
	22	46.2	4.4	1149	3	US-09-868-552-3	Sequence 3, Appli
	23	46.2	4.4	1149	3	US-09-868-552-5	Sequence 5, Appli
	24	46.2	4.4	1149	3	US-09-868-552-11	Sequence 11, Appl
	25	46.2	4.4	1149	3	US-09-868-552-13	Sequence 13, Appl
	26	46.2	4.4	1149	3	US-09-868-552-25	Sequence 25, Appl
	27	46.2	4.4	1540	3	US-09-868-552-24	Sequence 24, Appl
	28	46	4.3	601	3	US-09-949-016-198656	Sequence 198656,
c	29	45.2	4.3	2637	3	US-10-104-047-681	Sequence 681, App
	30	44.6	4.2	962	3	US-09-868-552-45	Sequence 45, Appl
	31	44.6	4.2	1149	3	US-09-868-552-9	Sequence 9, Appli
	32	44.6	4.2	1149	3	US-09-868-552-19	Sequence 19, Appl
	33	44.6	4.2	1149	3	US-09-868-552-22	Sequence 22, Appl
	34	44.6	4.2	1530	3	US-09-868-552-21	Sequence 21, Appl
	35	44.6	4.2	1540	3	US-09-868-552-18	Sequence 18, Appl
c	36	44.4	4.2	966	2	US-08-766-738-2	Sequence 2, Appli
c	37	44.4	4.2	966	3	US-09-262-610-2	Sequence 2, Appli
c	38	44.2	4.2	9636	2	US-08-323-170B-1	Sequence 1, Appli
c	39	44.2	4.2	9636	3	US-08-954-441-1	Sequence 1, Appli
c	40	43.4	4.1	19383	3	US-09-949-016-16031	Sequence 16031, A
	41	43	4.0	1149	3	US-09-868-552-7	Sequence 7, Appli
	42	43	4.0	1149	3	US-09-868-552-16	Sequence 16, Appl
	43	43	4.0	1270	3	US-08-387-805-1	Sequence 1, Appli
	44	43	4.0	1530	3	US-09-868-552-15	Sequence 15, Appl
	45	43	4.0	1633	2	US-07-866-979-5	Sequence 5, Appli

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:54:08 ; Search time 2724.59 Seconds
(without alignments)
4789.512 Million cell updates/sec

Title: US-09-995-225B-15
Perfect score: 1062
Sequence: 1 atggagcacacgcacgcca.....ctataaaagtatccccgtga 1062

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1062	100.0	1062	3	US-09-995-225-15	Sequence 15, Appl
2	1062	100.0	1062	3	US-09-995-225-15	Sequence 15, Appl
3	1062	100.0	1062	8	US-10-296-294A-4	Sequence 4, Appli
4	1062	100.0	2117	8	US-10-779-104-1	Sequence 1, Appli
5	1060.4	99.8	1062	8	US-10-296-294A-3	Sequence 3, Appli
6	1060.4	99.8	1202	6	US-10-094-417-1	Sequence 1, Appli
7	1060.4	99.8	1202	13	US-11-086-846-1	Sequence 1, Appli
8	1060	99.8	1776	10	US-10-505-486-210	Sequence 210, App
9	1058.8	99.7	1343	3	US-09-813-432-21	Sequence 21, Appl
10	1058.8	99.7	1343	7	US-10-174-364-21	Sequence 21, Appl
11	1058.8	99.7	1343	8	US-10-246-583-21	Sequence 21, Appl
12	1058.8	99.7	1343	8	US-10-689-832-21	Sequence 21, Appl
13	1057.4	99.6	1059	8	US-10-450-590-1	Sequence 1, Appli
14	1050.8	98.9	1062	6	US-10-012-140-12	Sequence 12, Appl
15	1050.8	98.9	1062	16	US-11-206-587-12	Sequence 12, Appl
16	1050.8	98.9	1526	6	US-10-012-140-10	Sequence 10, Appl
17	1050.8	98.9	1526	16	US-11-206-587-10	Sequence 10, Appl
18	1048.4	98.7	1119	3	US-09-813-432-19	Sequence 19, Appl
19	1048.4	98.7	1119	7	US-10-174-364-19	Sequence 19, Appl
20	1048.4	98.7	1119	8	US-10-246-583-19	Sequence 19, Appl
21	1048.4	98.7	1119	8	US-10-689-832-19	Sequence 19, Appl
22	1048.4	98.7	1130	8	US-10-333-946-25	Sequence 25, Appl
23	1048.4	98.7	2198	7	US-10-314-076-1	Sequence 1, Appli
24	1039.8	97.9	1110	7	US-10-314-076-3	Sequence 3, Appli
25	1039.8	97.9	2189	6	US-10-219-834-6	Sequence 6, Appli
26	945.2	89.0	1062	8	US-10-450-590-9	Sequence 9, Appli
27	940.2	88.5	957	7	US-10-174-364-84	Sequence 84, Appl
28	940.2	88.5	957	8	US-10-246-583-84	Sequence 84, Appl
29	936.4	88.2	1002	6	US-10-079-384-25	Sequence 25, Appl
30	936.4	88.2	1158	8	US-10-343-650A-21	Sequence 21, Appl
31	936.4	88.2	1167	10	US-10-745-237-375	Sequence 375, App
c 32	936.4	88.2	2694	4	US-09-925-065A-686393	Sequence 686393,
c 33	936.4	88.2	2694	5	US-09-925-065A-686393	Sequence 686393,
34	936	88.1	1032	8	US-10-450-590-5	Sequence 5, Appli
35	936	88.1	1070	8	US-10-450-590-4	Sequence 4, Appli
36	936	88.1	1826	8	US-10-450-590-6	Sequence 6, Appli
37	934.8	88.0	1000	10	US-10-297-990A-1	Sequence 1, Appli
38	844	79.5	1038	6	US-10-094-417-19	Sequence 19, Appl
39	844	79.5	1038	13	US-11-086-846-19	Sequence 19, Appl
c 40	842.6	79.3	864	3	US-09-791-932-6	Sequence 6, Appli
c 41	842.6	79.3	864	10	US-10-980-388-6	Sequence 6, Appli
42	758	71.4	795	6	US-10-225-567A-586	Sequence 586, App
43	532.6	50.2	609	4	US-09-925-065A-790337	Sequence 790337,
44	532.6	50.2	609	5	US-09-925-065A-790337	Sequence 790337,
c 45	524	49.3	930	3	US-09-791-932-3	Sequence 3, Appli

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b- 15.rnpbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 09995225 and Search Result us-09-995-225b-15.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:58:14 ; Search time 398.488 Seconds
(without alignments)
4343.677 Million cell updates/sec

Title: US-09-995-225B-15
Perfect score: 1062
Sequence: 1 atggagcàcacgcacgcca.....ctataaaagtatccccgtga 1062

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2239192 seqs, 814926892 residues

Total number of hits satisfying chosen parameters: 4478384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
- 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	985.6	92.8	1000	8	US-11-266-748A-394001	Sequence 394001,
c	2	985.6	92.8	1000	8	US-11-266-748A-465047	Sequence 465047,
	3	54	5.1	181179	8	US-11-266-748A-61130	Sequence 61130, A
c	4	53.8	5.1	895	9	US-11-056-355B-22685	Sequence 22685, A
	5	53	5.0	939	9	US-11-056-355B-80801	Sequence 80801, A
c	6	52.6	5.0	191010	6	US-10-533-595-7	Sequence 7, Appli
	7	49.6	4.7	1264	9	US-11-218-305-5220	Sequence 5220, Ap
c	8	49.6	4.7	2834	8	US-11-266-748A-23491	Sequence 23491, A
	9	47.8	4.5	2307	6	US-10-449-902-13869	Sequence 13869, A
c	10	47.4	4.5	772	6	US-10-953-349-39962	Sequence 39962, A
c	11	45	4.2	876	6	US-10-449-902-23639	Sequence 23639, A
c	12	44.6	4.2	1344	9	US-11-056-355B-70617	Sequence 70617, A
	13	44.6	4.2	2314	6	US-10-539-228-165	Sequence 165, App
	14	44.6	4.2	2579	8	US-11-216-545-4994	Sequence 4994, Ap
	15	44.6	4.2	22314	6	US-10-539-228-164	Sequence 164, App
c	16	44.4	4.2	713	8	US-11-266-748A-60911	Sequence 60911, A
c	17	44.4	4.2	2030	9	US-11-218-305-2019	Sequence 2019, Ap
c	18	43.8	4.1	1162	9	US-11-218-305-8276	Sequence 8276, Ap
c	19	43.8	4.1	1162	9	US-11-056-355B-8643	Sequence 8643, Ap
c	20	43.8	4.1	1162	9	US-11-056-355B-11574	Sequence 11574, A
c	21	43.6	4.1	892	9	US-11-056-355B-1063	Sequence 1063, Ap
c	22	43.4	4.1	958	6	US-10-953-349-35887	Sequence 35887, A
c	23	43.4	4.1	958	9	US-11-056-355B-4183	Sequence 4183, Ap
c	24	43.4	4.1	958	9	US-11-056-355B-12169	Sequence 12169, A
c	25	43.4	4.1	958	9	US-11-056-355B-19690	Sequence 19690, A
	26	43.4	4.1	976	9	US-11-218-305-20333	Sequence 20333, A
c	27	43.2	4.1	998	8	US-11-266-748A-19610	Sequence 19610, A
c	28	43.2	4.1	1000	8	US-11-266-748A-287316	Sequence 287316,
	29	43.2	4.1	1000	8	US-11-266-748A-338745	Sequence 338745,
c	30	43.2	4.1	1000	8	US-11-266-748A-397974	Sequence 397974,
	31	43.2	4.1	1000	8	US-11-266-748A-469020	Sequence 469020,
c	32	43.2	4.1	1055	8	US-11-266-748A-194196	Sequence 194196,
c	33	43.2	4.1	1055	8	US-11-266-748A-227714	Sequence 227714,
c	34	43.2	4.1	2024	9	US-11-218-305-14304	Sequence 14304, A
	35	43	4.0	951	8	US-11-257-851A-70	Sequence 70, Appl
c	36	42.6	4.0	1773	8	US-11-217-529-78093	Sequence 78093, A
	37	42	4.0	2001	6	US-10-449-902-8417	Sequence 8417, Ap
	38	42	4.0	2149	6	US-10-449-902-17995	Sequence 17995, A
	39	42	4.0	2553	9	US-11-218-305-20332	Sequence 20332, A
	40	41.4	3.9	1000	8	US-11-266-748A-287715	Sequence 287715,
c	41	41.4	3.9	1000	8	US-11-266-748A-339144	Sequence 339144,
	42	41.4	3.9	1000	8	US-11-266-748A-398468	Sequence 398468,
c	43	41.4	3.9	1000	8	US-11-266-748A-469514	Sequence 469514,
	44	41.4	3.9	1745	8	US-11-266-748A-26968	Sequence 26968, A
	45	41.4	3.9	1968	6	US-10-449-902-27797	Sequence 27797, A

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b- 15.rst.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 09995225 and Search Result us-09-995-225b-15.rst.

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:33:29 ; Search time 9061.32 Seconds
(without alignments)
6553.828 Million cell updates/sec

Title: US-09-995-225B-15
Perfect score: 1062
Sequence: 1 atggagcacacgcacgccca.....ctataaaagtatccccgtga 1062

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	No.	Score	Query Match	Length	DB	ID	
c	1	469.8	44.2	803	12	CC905917	CC905917 t025o11ba
	2	454.4	42.8	767	9	DN693347	DN693347 AGENCOURT
c	3	262	24.7	362	11	AZ513631	AZ513631 1M0359L07
c	4	241.4	22.7	448	11	AQ225693	AQ225693 HS_2009_B
	5	235	22.1	803	9	DN071254	DN071254 JGI_CABD6
	6	218.8	20.6	813	11	BZ169352	BZ169352 CH230-259
	7	209.8	19.8	806	14	CNS022E4	AL178069 Tetraodon
c	8	200	18.8	588	11	AQ344035	AQ344035 RPCI11-12
c	9	197	18.5	603	11	AQ351433	AQ351433 RPCI11-11
	10	195.8	18.4	321	10	DR896878	DR896878 JGI_XZT40
	11	187.6	17.7	947	14	CNS02BVQ	AL190367 Tetraodon
	12	185	17.4	708	3	BU610327	BU610327 UI-M-DJ2-
	13	183	17.2	824	12	CL137737	CL137737 ISB1-110A
	14	181	17.0	483	9	DA784027	DA784027 DA784027
	15	172.4	16.2	1269	13	CL649540	CL649540 CH213-237
	16	150	14.1	867	12	CL137848	CL137848 ISB1-110C
	17	149	14.0	898	14	CNS02ENP	AL193966 Tetraodon
	18	112.6	10.6	515	1	AL921815	AL921815 AL921815
	19	111.8	10.5	1107	14	CNS04L7F	AL295764 Tetraodon
	20	87.6	8.2	816	11	AZ535744	AZ535744 ENTCQ25TR
c	21	81.6	7.7	891	11	AZ683582	AZ683582 ENTKK47TR
	22	81.6	7.7	906	11	BH153606	BH153606 ENTTS83TF
	23	77.8	7.3	843	11	AZ551618	AZ551618 ENTDV54TR
c	24	77.4	7.3	908	11	AZ548467	AZ548467 ENTEK30TR
	25	75.4	7.1	616	14	DE228420	DE228420 Trifolium
	26	75	7.1	621	14	DE228276	DE228276 Trifolium
c	27	75	7.1	890	11	BH146886	BH146886 ENTPK48TF
	28	71.8	6.8	493	14	DE227254	DE227254 Trifolium
c	29	71.8	6.8	900	11	AZ549980	AZ549980 ENTDD94TF
c	30	71	6.7	976	11	BH149983	BH149983 ENTQD93TF
	31	70.8	6.7	580	14	DE226347	DE226347 Trifolium
	32	70.2	6.6	358	7	BB870915	BB870915 BB870915
	33	69.4	6.5	568	14	DE214279	DE214279 Trifolium
	34	69.2	6.5	877	11	AZ531291	AZ531291 ENTBQ34TR
c	35	69.2	6.5	912	11	AZ551092	AZ551092 ENTFJ22TF
	36	68.2	6.4	516	14	DE238899	DE238899 Trifolium
	37	68	6.4	449	14	DE225295	DE225295 Trifolium
	38	68	6.4	504	7	BB939286	BB939286 BB939286
	39	67.8	6.4	488	14	FR0012324	AL003576 F.rubripe
	40	67.6	6.4	888	11	AZ528430	AZ528430 ENTCO24TR
	41	67.4	6.3	849	11	AZ546009	AZ546009 ENTFW53TF
c	42	67.2	6.3	560	8	CX096334	CX096334 EHAGQ49TR
	43	67	6.3	539	14	DE225893	DE225893 Trifolium
	44	67	6.3	905	11	AZ550256	AZ550256 ENTEV58TR
	45	66.2	6.2	721	3	BW141179	BW141179 BW141179

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:30:29 ; Search time 201.749 Seconds
(without alignments)
8558.076 Million cell updates/sec

Title: US-09-995-225B-41
Perfect score: 27
Sequence: 1 gcgctcatggagcacacgcacgcccac 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match Length DB	ID	Description
	1	27	100.0 27 2	AX498218	AX498218 Sequence
	2	27	100.0 1130 2	AX375235	AX375235 Sequence
	3	27	100.0 1167 5	AY635179	AY635179 Homo sapi
	4	27	100.0 1526 2	AX664701	AX664701 Sequence
	5	27	100.0 2117 2	CQ867782	CQ867782 Sequence
c	6	27	100.0 101882 5	AC021089	AC021089 Homo sapi
c	7	27	100.0 110000 12	AL139235_0	AL139235 Homo sapi

c	8	27	100.0	140885	12	AC119798	AC119798 Rattus no
	9	27	100.0	183326	6	AC124438	AC124438 Mus muscu
c	10	27	100.0	196833	12	AC164864	AC164864 Bos tauru
	11	27	100.0	202934	6	AC147502	AC147502 Mus muscu
c	12	27	100.0	230813	12	AC114097	AC114097 Rattus no
c	13	22.8	84.4	110000	12	AP006494_2	Continuation (3 of
	14	22	81.5	32	2	BD103849	BD103849 Novel G p
	15	22	81.5	32	2	BD183201	BD183201 Novel G p
	16	21	77.8	1038	6	AB196531	AB196531 Rattus no
	17	21	77.8	1038	6	AB196532	AB196532 Mus muscu
	18	21	77.8	1038	6	AY485344	AY485344 Mus muscu
	19	21	77.8	1059	2	AX463227	AX463227 Sequence
	20	21	77.8	1062	2	BD103851	BD103851 Novel G p
	21	21	77.8	1062	2	BD103852	BD103852 Novel G p
	22	21	77.8	1062	2	BD183203	BD183203 Novel G p
	23	21	77.8	1062	2	BD183204	BD183204 Novel G p
	24	21	77.8	1062	2	AX463235	AX463235 Sequence
	25	21	77.8	1062	2	AX498192	AX498192 Sequence
	26	21	77.8	1062	2	AX664703	AX664703 Sequence
	27	21	77.8	1062	5	AB196529	AB196529 Homo sapi
	28	21	77.8	1119	2	AX254975	AX254975 Sequence
	29	21	77.8	1343	2	AX254977	AX254977 Sequence
c	30	20.6	76.3	828	7	BV680346	BV680346 TNFSF14_v
c	31	20.6	76.3	846	7	BV166828	BV166828 TNFSF14_1
c	32	20.6	76.3	110000	15	CP000076_13	Continuation (14 o
	33	20.4	75.6	110000	12	CR954217_1	Continuation (2 of
	34	20.2	74.8	1398	2	AX934641	AX934641 Sequence
	35	20.2	74.8	180230	12	CT030237	CT030237 Danio rer
	36	20.2	74.8	181788	12	CR396589	CR396589 Danio rer
c	37	19.8	73.3	664	5	HSA341042	AJ341042 Homo sapi
	38	19.8	73.3	3796	2	AX151499	AX151499 Sequence
	39	19.8	73.3	10321	15	AE012251	AE012251 Xanthomon
	40	19.8	73.3	110000	12	CR954208_5	Continuation (6 of
	41	19.8	73.3	110000	12	CT005252_0	CT005252 Leishmani
c	42	19.8	73.3	110000	15	CP000050_32	Continuation (33 o
c	43	19.8	73.3	130500	12	AC148130	AC148130 Carollia
c	44	19.8	73.3	170415	12	AC123299	AC123299 Rattus no
	45	19.8	73.3	292967	10	AF369029	AF369029 White spo

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b- 41.rng.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 09995225 and Search Result us-09-995-225b-41.rng.

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:24:07 ; Search time 28.9147 Seconds
(without alignments)
6510.549 Million cell updates/sec

Title: US-09-995-225B-41
Perfect score: 27
Sequence: 1 gcgctcatggagcacacgcacgcccac 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	100.0	27	6	ABT04896	Abt04896 Human G p
2	27	100.0	1130	6	AAD29672	Aad29672 Human G-p
3	27	100.0	1202	8	ABV73364	Abv73364 Human TGR
4	27	100.0	1526	6	AAD46858	Aad46858 Human 7TM
5	27	100.0	1526	8	ACA60889	Aca60889 Human cDN
6	27	100.0	1526	10	ABS57024	Abs57024 cDNA enco
7	27	100.0	2117	13	ADR16433	Adr16433 Human KOR
8	27	100.0	2189	10	ADD18120	Add18120 Human G-p
9	27	100.0	2198	9	ACF05275	Acf05275 Human G-p
10	27	100.0	2273	12	ADO28955	Ado28955 Human nov
11	22	81.5	32	6	ABK15560	Abk15560 Novel G-p
12	22	81.5	42	10	ADJ87864	Adj87864 G-coupled
13	22	81.5	42	12	ADO56045	Ado56045 Human NOV
14	21	77.8	25	12	ADO30468	Ado30468 Human nov
15	21	77.8	28	10	ACC71787	Acc71787 Human G p
16	21	77.8	116	10	ACC71795	Acc71795 Human G p
17	21	77.8	1038	8	ABV73373	Abv73373 Mouse TGR
18	21	77.8	1038	12	ADO28957	Ado28957 Mouse nov
19	21	77.8	1059	6	ABN84269	Abn84269 Human che
20	21	77.8	1062	6	ABK15562	Abk15562 cDNA enco
21	21	77.8	1062	6	ABK15563	Abk15563 cDNA enco
22	21	77.8	1062	6	ABT04873	Abt04873 Human G p
23	21	77.8	1062	6	ABN84273	Abn84273 Human che
24	21	77.8	1062	10	ACC44115	Acc44115 Human AXO
25	21	77.8	1062	10	ACC71785	Acc71785 Human G p
26	21	77.8	1110	9	ACF05276	Acf05276 Human G-p
27	21	77.8	1119	4	AAS15730	Aas15730 DNA encod
28	21	77.8	1119	10	ADJ87766	Adj87766 G-coupled
29	21	77.8	1119	12	ADI79322	Adi79322 NOV10a co
30	21	77.8	1119	12	ADO56001	Ado56001 DNA encod
31	21	77.8	1343	4	AAS15731	Aas15731 DNA encod
32	21	77.8	1343	10	ADJ87768	Adj87768 G-coupled
33	21	77.8	1343	12	ADI79324	Adi79324 NOV11 cod
34	21	77.8	1343	12	ADO56003	Ado56003 DNA encod
35	21	77.8	1776	10	ADF70587	Adf70587 Orphan re
36	20.2	74.8	1398	10	ADG33813	Adg33813 Actinomyc
37	19.8	73.3	3796	4	AAH62741	Aah62741 Shrimp wh
38	19.8	73.3	305107	4	AAH62689	Aah62689 Shrimp wh
c 39	19.6	72.6	178	10	ADJ81026	Adj81026 INSP010 n
40	19.6	72.6	1365	14	AED46552	Aed46552 Cellobioh
c 41	19.6	72.6	8676	10	ADJ81128	Adj81128 INSP010 m
c 42	19.6	72.6	8742	10	ADJ81122	Adj81122 INSP010 n
c 43	19.6	72.6	8838	6	ABV99367	Abv99367 Human NOV
c 44	19.6	72.6	8862	10	ADJ81136	Adj81136 INSP010 p
45	19.6	72.6	349980	6	ABQ81849	Abq81849 Bifidobac

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b- 41.rni.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:44:27 ; Search time 9.21005 Seconds
(without alignments)
5485.303 Million cell updates/sec

Title: US-09-995-225B-41
Perfect score: 27
Sequence: 1 gcgctcatggagcacacgcacgcccac 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	19	70.4	601	3	US-09-949-016-193101	Sequence 193101,	
2	19	70.4	601	3	US-09-949-016-193194	Sequence 193194,	
3	19	70.4	601	3	US-09-949-016-193287	Sequence 193287,	
4	19	70.4	601	3	US-09-949-016-193380	Sequence 193380,	
c 5	19	70.4	720	3	US-08-913-014A-4	Sequence 4, Appli	
c 6	19	70.4	720	3	US-09-653-285-4	Sequence 4, Appli	
c 7	19	70.4	810	3	US-09-072-993C-5	Sequence 5, Appli	
c 8	19	70.4	1017	3	US-09-027-287-38	Sequence 38, Appl	
c 9	19	70.4	1017	3	US-09-252-656B-38	Sequence 38, Appl	
c 10	19	70.4	1017	3	US-09-523-323-38	Sequence 38, Appl	
c 11	19	70.4	1169	3	US-09-027-287-1	Sequence 1, Appli	
c 12	19	70.4	1169	3	US-09-252-656B-1	Sequence 1, Appli	
c 13	19	70.4	1169	3	US-09-523-323-1	Sequence 1, Appli	
c 14	19	70.4	1353	3	US-08-913-014A-6	Sequence 6, Appli	
c 15	19	70.4	1353	3	US-09-653-285-6	Sequence 6, Appli	
c 16	19	70.4	1491	3	US-08-913-014A-5	Sequence 5, Appli	
c 17	19	70.4	1491	3	US-09-653-285-5	Sequence 5, Appli	
c 18	19	70.4	2358	3	US-09-902-540-2632	Sequence 2632, Ap	
c 19	19	70.4	17173	3	US-09-902-540-1122	Sequence 1122, Ap	
20	19	70.4	86213	3	US-09-949-016-17240	Sequence 17240, A	
21	19	70.4	86213	3	US-09-949-016-17241	Sequence 17241, A	
22	19	70.4	86213	3	US-09-949-016-17242	Sequence 17242, A	
23	19	70.4	86213	3	US-09-949-016-17243	Sequence 17243, A	
c 24	18.6	68.9	1533	3	US-09-270-767-12691	Sequence 12691, A	
c 25	18.6	68.9	4521	3	US-09-902-540-3633	Sequence 3633, Ap	
26	18.6	68.9	9369	3	US-10-237-551-190	Sequence 190, App	
27	18.6	68.9	9369	3	US-10-237-551-247	Sequence 247, App	
c 28	18.6	68.9	19269	3	US-09-902-540-1175	Sequence 1175, Ap	
c 29	18.6	68.9	154746	3	US-09-827-688-8	Sequence 8, Appli	
30	18.2	67.4	1458	3	US-10-011-200-1	Sequence 1, Appli	
31	18.2	67.4	2346	3	US-10-011-200-2	Sequence 2, Appli	
32	18	66.7	438	3	US-09-060-756-600	Sequence 600, App	
33	18	66.7	438	3	US-09-670-314-600	Sequence 600, App	
34	18	66.7	438	4	US-10-259-678-600	Sequence 600, App	
35	18	66.7	492	3	US-09-060-756-587	Sequence 587, App	
36	18	66.7	492	3	US-09-670-314-587	Sequence 587, App	
37	18	66.7	492	4	US-10-259-678-587	Sequence 587, App	
38	18	66.7	1423	2	US-08-386-729A-6	Sequence 6, Appli	
c 39	18	66.7	2259	3	US-09-489-039A-3024	Sequence 3024, Ap	
c 40	18	66.7	3492	3	US-09-902-540-3089	Sequence 3089, Ap	
c 41	18	66.7	10717	3	US-09-902-540-991	Sequence 991, App	
c 42	18	66.7	15789	3	US-09-902-540-1139	Sequence 1139, Ap	
c 43	18	66.7	35007	3	US-09-949-016-15330	Sequence 15330, A	
c 44	18	66.7	166698	3	US-09-949-016-16038	Sequence 16038, A	
45	18	66.7	190078	3	US-09-949-016-12707	Sequence 12707, A	

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b- 41.rnpbm.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:54:08 ; Search time 69.2693 Seconds
(without alignments)
4789.512 Million cell updates/sec

Title: US-09-995-225B-41
Perfect score: 27
Sequence: 1 gcgctcatggagcacacgcacgcccac 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	100.0	27	3	US-09-995-225-41	Sequence 41, Appl
2	27	100.0	27	3	US-09-995-225-41	Sequence 41, Appl
3	27	100.0	1130	8	US-10-333-946-25	Sequence 25, Appl
4	27	100.0	1202	6	US-10-094-417-1	Sequence 1, Appli
5	27	100.0	1202	13	US-11-086-846-1	Sequence 1, Appli
6	27	100.0	1526	6	US-10-012-140-10	Sequence 10, Appl
7	27	100.0	1526	16	US-11-206-587-10	Sequence 10, Appl
8	27	100.0	2117	8	US-10-779-104-1	Sequence 1, Appli
9	27	100.0	2189	6	US-10-219-834-6	Sequence 6, Appli
10	27	100.0	2198	7	US-10-314-076-1	Sequence 1, Appli
11	22	81.5	32	8	US-10-296-294A-1	Sequence 1, Appli
12	22	81.5	42	7	US-10-174-364-117	Sequence 117, App
13	22	81.5	42	8	US-10-246-583-117	Sequence 117, App
14	21	77.8	1038	6	US-10-094-417-19	Sequence 19, Appl
15	21	77.8	1038	13	US-11-086-846-19	Sequence 19, Appl
16	21	77.8	1059	8	US-10-450-590-1	Sequence 1, Appli
17	21	77.8	1062	3	US-09-995-225-15	Sequence 15, Appl
18	21	77.8	1062	3	US-09-995-225-15	Sequence 15, Appl
19	21	77.8	1062	6	US-10-012-140-12	Sequence 12, Appl
20	21	77.8	1062	8	US-10-296-294A-3	Sequence 3, Appli
21	21	77.8	1062	8	US-10-296-294A-4	Sequence 4, Appli
22	21	77.8	1062	8	US-10-450-590-9	Sequence 9, Appli
23	21	77.8	1062	16	US-11-206-587-12	Sequence 12, Appl
24	21	77.8	1110	7	US-10-314-076-3	Sequence 3, Appli
25	21	77.8	1119	3	US-09-813-432-19	Sequence 19, Appl
26	21	77.8	1119	7	US-10-174-364-19	Sequence 19, Appl
27	21	77.8	1119	8	US-10-246-583-19	Sequence 19, Appl
28	21	77.8	1119	8	US-10-689-832-19	Sequence 19, Appl
29	21	77.8	1343	3	US-09-813-432-21	Sequence 21, Appl
30	21	77.8	1343	7	US-10-174-364-21	Sequence 21, Appl
31	21	77.8	1343	8	US-10-246-583-21	Sequence 21, Appl
32	21	77.8	1343	8	US-10-689-832-21	Sequence 21, Appl
33	21	77.8	1776	10	US-10-505-486-210	Sequence 210, App
34	20.6	76.3	1530	9	US-10-425-115-115292	Sequence 115292,
35	20.2	74.8	1398	8	US-10-417-700A-72	Sequence 72, Appl
c 36	19.6	72.6	8838	7	US-10-093-463-81	Sequence 81, Appl
37	19.6	72.6	2256646	8	US-10-470-565-1	Sequence 1, Appli
c 38	19	70.4	600	10	US-10-750-185-3026	Sequence 3026, Ap
c 39	19	70.4	600	10	US-10-750-623-3026	Sequence 3026, Ap
c 40	19	70.4	612	8	US-10-468-161-30	Sequence 30, Appl
c 41	19	70.4	612	10	US-10-982-442A-30	Sequence 30, Appl
c 42	19	70.4	612	16	US-11-136-341A-30	Sequence 30, Appl
43	19	70.4	672	9	US-10-425-115-169941	Sequence 169941,
c 44	19	70.4	720	8	US-10-468-161-4	Sequence 4, Appli
c 45	19	70.4	720	10	US-10-982-442A-4	Sequence 4, Appli

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b- 41.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:58:14 ; Search time 10.1311 Seconds
(without alignments)
4343.677 Million cell updates/sec

Title: US-09-995-225B-41
Perfect score: 27
Sequence: 1 gcgctcatggagcacacgcacgcccac 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2239192 seqs, 814926892 residues

Total number of hits satisfying chosen parameters: 4478384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
- 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20.6	76.3	912	9	US-11-218-305-12656	Sequence 12656, A
2	20.6	76.3	1530	9	US-11-218-305-12269	Sequence 12269, A
c 3	19	70.4	748	8	US-11-266-748A-264816	Sequence 264816,
4	19	70.4	748	8	US-11-266-748A-325333	Sequence 325333,
c 5	19	70.4	748	8	US-11-266-748A-370605	Sequence 370605,
6	19	70.4	748	8	US-11-266-748A-453984	Sequence 453984,
c 7	19	70.4	887	8	US-11-266-748A-247827	Sequence 247827,
c 8	19	70.4	1000	8	US-11-266-748A-405049	Sequence 405049,
9	19	70.4	1000	8	US-11-266-748A-476095	Sequence 476095,
10	19	70.4	1124	6	US-10-449-902-22927	Sequence 22927, A
11	19	70.4	1183	6	US-10-449-902-11996	Sequence 11996, A
12	19	70.4	1395	8	US-11-266-748A-31387	Sequence 31387, A
13	19	70.4	1589	6	US-10-449-902-4688	Sequence 4688, Ap
14	19	70.4	1835	6	US-10-449-902-14648	Sequence 14648, A
15	19	70.4	126068	8	US-11-257-817-31	Sequence 31, Appl
16	18.6	68.9	1878	6	US-10-449-902-11800	Sequence 11800, A
c 17	18.6	68.9	208765	6	US-10-540-898-407	Sequence 407, App
18	18.2	67.4	1560	9	US-11-218-305-16825	Sequence 16825, A
19	18	66.7	776	9	US-11-056-355B-10233	Sequence 10233, A
20	17.6	65.2	918	8	US-11-266-748A-18526	Sequence 18526, A
21	17.6	65.2	1000	8	US-11-266-748A-408347	Sequence 408347,
c 22	17.6	65.2	1000	8	US-11-266-748A-479393	Sequence 479393,
23	17.6	65.2	1645	6	US-10-449-902-8349	Sequence 8349, Ap
c 24	17.6	65.2	3258	8	US-11-266-748A-30828	Sequence 30828, A
c 25	17.6	65.2	4612	9	US-11-218-305-5691	Sequence 5691, Ap
c 26	17.6	65.2	5827	9	US-11-218-305-3854	Sequence 3854, Ap
27	17.4	64.4	775	6	US-10-449-902-10656	Sequence 10656, A
28	17.4	64.4	788	6	US-10-449-902-13661	Sequence 13661, A
29	17.4	64.4	944	6	US-10-449-902-21041	Sequence 21041, A
c 30	17.4	64.4	972	9	US-11-056-355B-4000	Sequence 4000, Ap
c 31	17.4	64.4	1000	8	US-11-266-748A-117931	Sequence 117931,
32	17.4	64.4	1000	8	US-11-266-748A-160095	Sequence 160095,
c 33	17.4	64.4	1000	8	US-11-266-748A-290575	Sequence 290575,
34	17.4	64.4	1000	8	US-11-266-748A-342004	Sequence 342004,
c 35	17.4	64.4	1000	8	US-11-266-748A-401878	Sequence 401878,
36	17.4	64.4	1000	8	US-11-266-748A-472924	Sequence 472924,
37	17.4	64.4	1030	6	US-10-953-349-38884	Sequence 38884, A
38	17.4	64.4	1044	9	US-11-174-307B-3939	Sequence 3939, Ap
c 39	17.4	64.4	1057	9	US-11-056-355B-3678	Sequence 3678, Ap
40	17.4	64.4	1164	9	US-11-218-305-12658	Sequence 12658, A
41	17.4	64.4	1200	9	US-11-056-355B-15850	Sequence 15850, A
c 42	17.4	64.4	1217	9	US-11-218-305-3369	Sequence 3369, Ap
43	17.4	64.4	1276	9	US-11-056-355B-621	Sequence 621, App
44	17.4	64.4	1319	9	US-11-218-305-12657	Sequence 12657, A
45	17.4	64.4	1362	9	US-11-218-305-12655	Sequence 12655, A

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b- 41.rst.

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:33:29 ; Search time 230.373 Seconds
(without alignments)
6553.828 Million cell updates/sec

Title: US-09-995-225B-41
Perfect score: 27
Sequence: 1 gcgctcatggagcacacgcacgcccac 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query				DB	ID	Description
No.	Score	Match	Length						
1	27	100.0	358	7	BB870915			BB870915	BB870915
2	27	100.0	483	9	DA784027			DA784027	DA784027
3	27	100.0	767	9	DN693347			DN693347	AGENCOURT
c 4	20.8	77.0	843	5	CJ433301			CJ433301	CJ433301
c 5	20.6	76.3	660	13	DU258730			DU258730	109857418
6	20.6	76.3	693	7	BF430732			BF430732	OG04A11T3
7	20.6	76.3	753	10	DT946830			DT946830	ZM_BFb013
8	20.6	76.3	771	12	CC340173			CC340173	OGUAE29TH
c 9	20.6	76.3	786	3	BU207814			BU207814	603102460
c 10	20.6	76.3	818	13	DU291751			DU291751	109841599
11	20.6	76.3	825	12	BZ714949			BZ714949	PUFAD34TD
12	20.6	76.3	848	10	DT652346			DT652346	ZM_BFb011
13	20.6	76.3	973	10	DV853564			DV853564	col824 Co
c 14	20.2	74.8	109	12	CC396746			CC396746	PUHDZ11TB
c 15	20.2	74.8	539	3	BQ143379			BQ143379	fmh1c.pk0
c 16	19.6	72.6	342	10	DV080433			DV080433	MGC9.7.1.
c 17	19.6	72.6	356	4	BY324213			BY324213	BY324213
18	19.6	72.6	412	4	CB388569			CB388569	OSTF101D3
19	19.6	72.6	436	10	DV080434			DV080434	MGC9.7.1.
c 20	19.6	72.6	455	11	AQ557735			AQ557735	HS_2083_A
21	19.6	72.6	490	11	AQ177428			AQ177428	HS_2206_A
22	19.6	72.6	504	11	AZ446249			AZ446249	1M0242A10
23	19.6	72.6	599	7	AW057282			AW057282	ca03c06.y
24	19.6	72.6	617	4	CB469087			CB469087	sn03_A04.
c 25	19.6	72.6	623	11	AZ999005			AZ999005	2M0286N12
26	19.6	72.6	656	11	BZ308052			BZ308052	id35b05.b
c 27	19.6	72.6	680	12	CC714295			CC714295	OGWEV32TV
c 28	19.6	72.6	709	13	CZ256101			CZ256101	LQCX404TJ
29	19.6	72.6	784	11	BZ551201			BZ551201	pacs1-60_
30	19.6	72.6	810	11	BZ359952			BZ359952	id84d12.b
c 31	19.6	72.6	857	8	CN204077			CN204077	Tor4467 G
32	19.6	72.6	938	12	BZ570003			BZ570003	msh2_1120
33	19.6	72.6	951	12	CG093748			CG093748	PUFUE09TD
c 34	19.6	72.6	979	13	CW919389			CW919389	EDCAA58TF
c 35	19.6	72.6	988	12	CG093746			CG093746	PUFUE09TB
c 36	19.6	72.6	997	13	CW927488			CW927488	EDCBM11TF
c 37	19.6	72.6	1195	12	BZ579041			BZ579041	msh2_6143
38	19.6	72.6	1606	11	BZ556139			BZ556139	pacs1-60_
c 39	19.6	72.6	8523	14	AY405945			AY405945	Homo sapi
c 40	19.4	71.9	443	14	AG185710			AG185710	Pan trogl
41	19.4	71.9	514	10	DV538103			DV538103	ZM_BFb023
c 42	19.2	71.1	343	12	CE794750			CE794750	tigr-gss-
43	19.2	71.1	450	8	CV031010			CV031010	CS_gil_26
44	19.2	71.1	453	8	CV161690			CV161690	CS_gil_55
c 45	19.2	71.1	472	13	CW215549			CW215549	104_647_1

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:24:07 ; Search time 26.7729 Seconds
(without alignments)
6510.549 Million cell updates/sec

Title: US-09-995-225B-42
Perfect score: 25
Sequence: 1 gaggcagtagttgccacacctatgg 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*
- 15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match Length	DB	ID	Description	
	1	25	100.0	25	6	ABT04897	Abt04897 Human G p
c	2	25	100.0	1202	8	ABV73364	Abv73364 Human TGR
c	3	25	100.0	1343	4	AAS15731	Aas15731 DNA encod
c	4	25	100.0	1343	10	ADJ87768	Adj87768 G-coupled
c	5	25	100.0	1343	12	ADI79324	Adi79324 NOV11 cod
c	6	25	100.0	1343	12	ADO56003	Ado56003 DNA encod
c	7	25	100.0	1526	6	AAD46858	Aad46858 Human 7TM
c	8	25	100.0	1526	8	ACA60889	Aca60889 Human cDN
c	9	25	100.0	1526	10	ABS57024	Abs57024 cDNA enco
c	10	25	100.0	1826	6	ABN84272	Abn84272 Human che
c	11	25	100.0	2117	13	ADR16433	Adr16433 Human KOR
c	12	25	100.0	2273	12	ADO28955	Ado28955 Human nov
c	13	19.2	76.8	326663	14	AED18562	Aed18562 Fibrotic
c	14	18.2	72.8	295	4	AAH57320	Aah57320 Human pan
	15	18.2	72.8	147309	6	ABK49450	Abk49450 Human tra
c	16	17.6	70.4	879	4	AAI94220	Aai94220 Human neu
	17	17.6	70.4	1376	12	ADO60492	Ado60492 Chlamydom
	18	17.6	70.4	152501	12	ADP67269	Adp67269 Human chr
	19	17.4	69.6	208	5	ADI73980	Adi73980 Human ova
	20	17.4	69.6	208	5	ADI67597	Adi67597 Human ova
c	21	17.4	69.6	248	5	ADL45408	Adl45408 Human ova
c	22	17.4	69.6	350	3	AAC08203	Aac08203 Human sec
	23	17.4	69.6	527	5	ADL39217	Adl39217 Human ova
c	24	17.4	69.6	674	4	AAS31458	Aas31458 Human cDN
c	25	17.4	69.6	674	6	ABQ66782	Abq66782 Human pol
c	26	17.4	69.6	674	10	ADC10804	Adc10804 Human cDN
c	27	17.4	69.6	1182	6	ABZ22351	Abz22351 BM hepara
c	28	17.4	69.6	1596	10	ADF68972	Adf68972 Avian pne
c	29	17.4	69.6	1596	10	ADF89293	Adf89293 Avian pne
c	30	17.4	69.6	1596	12	ADJ96792	Adj96792 Avian pne
c	31	17.4	69.6	1596	12	ADL07739	Adl07739 Avian pne
c	32	17.4	69.6	1596	12	ADM67263	Adm67263 Avian pne
c	33	17.4	69.6	1596	13	ADU25764	Adu25764 Avian pne
c	34	17.4	69.6	1596	14	ADY84132	Ady84132 Avian pne
c	35	17.4	69.6	1614	3	AAA14952	Aaa14952 Nucleotid
c	36	17.4	69.6	1644	12	ADQ30909	Adq30909 Avian pne
c	37	17.4	69.6	1666	10	ADF68973	Adf68973 Avian pne
c	38	17.4	69.6	1666	10	ADF89294	Adf89294 Avian pne
c	39	17.4	69.6	1666	12	ADJ96793	Adj96793 DNA of th
c	40	17.4	69.6	1666	12	ADL07740	Adl07740 Avian pne
c	41	17.4	69.6	1666	12	ADM67264	Adm67264 Avian pne
c	42	17.4	69.6	1666	13	ADU25765	Adu25765 Avian pne
c	43	17.4	69.6	1666	14	ADY84133	Ady84133 Avian pne
c	44	17.4	69.6	1860	10	ADF68975	Adf68975 Avian pne
c	45	17.4	69.6	1860	10	ADF89296	Adf89296 Avian pne

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OM nucleic - nucleic search, using sw model

```
Run on:      August 24, 2006, 16:44:27 ; Search time 8.52783 Seconds
              (without alignments)
              5485.303 Million cell updates/sec
```

Title: US-09-995-225B-42
Perfect score: 25
Sequence: 1 gaqgcagtaqattgccacacctatqq 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Issued_Patents_NA:*
1:   /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2:   /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3:   /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4:   /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5:   /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6:   /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7:   /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8:   /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9:   /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10:  /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query						
No.	Score	Match	Length	DB	ID	Description		
c	1	18.8	75.2	601	3	US-09-949-016-81041	Sequence	81041, A
c	2	18.8	75.2	108440	3	US-09-949-016-12065	Sequence	12065, A
c	3	18.8	75.2	108441	3	US-09-949-016-14090	Sequence	14090, A
	4	18.2	72.8	601	3	US-09-949-016-188302	Sequence	188302, A
	5	18.2	72.8	601	3	US-09-949-016-188303	Sequence	188303, A
	6	18.2	72.8	158735	3	US-09-949-016-11989	Sequence	11989, A
	7	18.2	72.8	158735	3	US-09-949-016-17130	Sequence	17130, A
c	8	17.6	70.4	601	3	US-09-949-016-41906	Sequence	41906, A
	9	17.6	70.4	150409	3	US-09-949-016-12290	Sequence	12290, A
	10	17.6	70.4	150409	3	US-09-949-016-12938	Sequence	12938, A
c	11	17.4	69.6	350	3	US-09-513-999C-12278	Sequence	12278, A
c	12	17.4	69.6	2216	3	US-10-104-047-1368	Sequence	1368, Ap
	13	17.2	68.8	381	3	US-09-513-999C-13199	Sequence	13199, A
c	14	17.2	68.8	134292	3	US-09-949-016-12158	Sequence	12158, A
c	15	17.2	68.8	767677	3	US-09-949-016-12147	Sequence	12147, A
c	16	17.2	68.8	767677	3	US-09-949-016-17361	Sequence	17361, A
	17	17	68.0	601	3	US-09-949-016-22339	Sequence	22339, A
	18	17	68.0	601	3	US-09-949-016-92738	Sequence	92738, A
	19	17	68.0	601	3	US-09-949-016-92752	Sequence	92752, A
	20	17	68.0	601	3	US-09-949-016-92766	Sequence	92766, A
	21	17	68.0	601	3	US-09-949-016-92780	Sequence	92780, A
c	22	17	68.0	601	3	US-09-949-016-180763	Sequence	180763, A
c	23	17	68.0	984	3	US-09-902-540-3549	Sequence	3549, Ap
c	24	17	68.0	2129	3	US-09-949-016-214	Sequence	214, App
c	25	17	68.0	2131	3	US-09-949-016-2661	Sequence	2661, Ap
c	26	17	68.0	2131	3	US-09-949-016-2662	Sequence	2662, Ap
c	27	17	68.0	2131	3	US-09-949-016-3549	Sequence	3549, Ap
c	28	17	68.0	2131	3	US-09-949-016-3550	Sequence	3550, Ap
	29	17	68.0	2424	3	US-09-949-016-3566	Sequence	3566, Ap
c	30	17	68.0	5913	3	US-09-949-016-2035	Sequence	2035, Ap
	31	17	68.0	16704	3	US-09-949-016-15308	Sequence	15308, A
	32	17	68.0	17228	3	US-09-902-540-1170	Sequence	1170, Ap
c	33	17	68.0	19181	3	US-09-949-016-14405	Sequence	14405, A
c	34	17	68.0	19181	3	US-09-949-016-14406	Sequence	14406, A
c	35	17	68.0	20713	3	US-09-949-016-11956	Sequence	11956, A
c	36	17	68.0	20727	3	US-09-949-016-14403	Sequence	14403, A
c	37	17	68.0	20727	3	US-09-949-016-14404	Sequence	14404, A
c	38	17	68.0	20728	3	US-09-949-016-15291	Sequence	15291, A
c	39	17	68.0	20728	3	US-09-949-016-15292	Sequence	15292, A
	40	17	68.0	23902	3	US-09-949-016-14220	Sequence	14220, A
	41	17	68.0	24546	3	US-09-949-016-16638	Sequence	16638, A
c	42	17	68.0	43657	3	US-09-949-016-13777	Sequence	13777, A
c	43	17	68.0	67620	3	US-09-949-016-16939	Sequence	16939, A
c	44	17	68.0	422592	3	US-09-949-016-14182	Sequence	14182, A
c	45	16.8	67.2	62804	3	US-09-800-960-3	Sequence	3, Appli

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:54:08 ; Search time 64.1382 Seconds
(without alignments)
4789.512 Million cell updates/sec

Title: US-09-995-225B-42
Perfect score: 25
Sequence: 1 gaggcagtagttgccacacctatgg 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	25	100.0	25	3	US-09-995-225-42	Sequence 42, Appl
	2	25	100.0	25	3	US-09-995-225-42	Sequence 42, Appl
c	3	25	100.0	609	4	US-09-925-065A-790337	Sequence 790337,
c	4	25	100.0	609	5	US-09-925-065A-790337	Sequence 790337,
c	5	25	100.0	1202	6	US-10-094-417-1	Sequence 1, Appli
c	6	25	100.0	1202	13	US-11-086-846-1	Sequence 1, Appli
c	7	25	100.0	1343	3	US-09-813-432-21	Sequence 21, Appl
c	8	25	100.0	1343	7	US-10-174-364-21	Sequence 21, Appl
c	9	25	100.0	1343	8	US-10-246-583-21	Sequence 21, Appl
c	10	25	100.0	1343	8	US-10-689-832-21	Sequence 21, Appl
c	11	25	100.0	1526	6	US-10-012-140-10	Sequence 10, Appl
c	12	25	100.0	1526	16	US-11-206-587-10	Sequence 10, Appl
c	13	25	100.0	1826	8	US-10-450-590-6	Sequence 6, Appli
c	14	25	100.0	2117	8	US-10-779-104-1	Sequence 1, Appli
	15	25	100.0	2694	4	US-09-925-065A-686393	Sequence 686393,
	16	25	100.0	2694	5	US-09-925-065A-686393	Sequence 686393,
c	17	19.2	76.8	688	8	US-10-424-599-59902	Sequence 59902, A
c	18	18.8	75.2	992	12	US-10-301-480-610301	Sequence 610301,
c	19	18.8	75.2	992	12	US-10-301-480-1223710	Sequence 1223710,
c	20	18.6	74.4	2634	10	US-10-750-185-50342	Sequence 50342, A
c	21	18.6	74.4	2634	10	US-10-750-623-50342	Sequence 50342, A
	22	18.2	72.8	406	4	US-09-925-065A-911799	Sequence 911799,
	23	18.2	72.8	406	5	US-09-925-065A-911799	Sequence 911799,
c	24	18.2	72.8	428	4	US-09-925-065A-911818	Sequence 911818,
c	25	18.2	72.8	428	5	US-09-925-065A-911818	Sequence 911818,
c	26	18.2	72.8	826	10	US-10-750-185-60338	Sequence 60338, A
c	27	18.2	72.8	826	10	US-10-750-623-60338	Sequence 60338, A
c	28	18.2	72.8	1886	8	US-10-437-963-65084	Sequence 65084, A
	29	18.2	72.8	147309	3	US-09-742-312-3	Sequence 3, Appli
	30	18.2	72.8	147309	7	US-10-436-185-3	Sequence 3, Appli
	31	17.8	71.2	275	9	US-10-425-115-19752	Sequence 19752, A
	32	17.8	71.2	550	12	US-10-301-480-393463	Sequence 393463,
	33	17.8	71.2	550	12	US-10-301-480-1006872	Sequence 1006872,
c	34	17.8	71.2	552	4	US-09-925-065A-318645	Sequence 318645,
c	35	17.8	71.2	552	5	US-09-925-065A-318645	Sequence 318645,
	36	17.8	71.2	600	10	US-10-972-079-7780	Sequence 7780, Ap
c	37	17.8	71.2	787	8	US-10-767-701-14254	Sequence 14254, A
	38	17.6	70.4	457	12	US-10-301-480-224329	Sequence 224329,
	39	17.6	70.4	457	12	US-10-301-480-318627	Sequence 318627,
	40	17.6	70.4	457	12	US-10-301-480-318628	Sequence 318628,
	41	17.6	70.4	457	12	US-10-301-480-837738	Sequence 837738,
	42	17.6	70.4	457	12	US-10-301-480-932036	Sequence 932036,
	43	17.6	70.4	457	12	US-10-301-480-932037	Sequence 932037,
	44	17.6	70.4	463	4	US-09-925-065A-127204	Sequence 127204,
	45	17.6	70.4	463	4	US-09-925-065A-235947	Sequence 235947,

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:58:14 ; Search time 9.38061 Seconds
(without alignments)
4343.677 Million cell updates/sec

Title: US-09-995-225B-42
Perfect score: 25
Sequence: 1 gaggcagtagttgccacacctatgg 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2239192 seqs, 814926892 residues

Total number of hits satisfying chosen parameters: 4478384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
- 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				
No.	Score	Query	Match	Length	DB	ID	Description
	1	17.6	70.4	209216	8	US-11-266-748A-23277	Sequence 23277, A
c	2	17.4	69.6	1120	8	US-11-266-748A-366087	Sequence 366087,
	3	17.4	69.6	1120	8	US-11-266-748A-449466	Sequence 449466,
c	4	17.4	69.6	1276	8	US-11-266-748A-26870	Sequence 26870, A
c	5	17.4	69.6	1724	8	US-11-266-748A-96823	Sequence 96823, A
	6	17.4	69.6	1724	8	US-11-266-748A-149634	Sequence 149634,
	7	17.2	68.8	1043	6	US-10-449-902-11015	Sequence 11015, A
c	8	17.2	68.8	1714	8	US-11-216-545-600	Sequence 600, App
	9	17.2	68.8	3143	8	US-11-293-697-638	Sequence 638, App
	10	17.2	68.8	4134	9	US-11-348-413-6611	Sequence 6611, Ap
	11	17.2	68.8	5523	8	US-11-266-748A-24540	Sequence 24540, A
	12	17	68.0	261	8	US-11-266-748A-230092	Sequence 230092,
c	13	17	68.0	726	8	US-11-266-748A-169032	Sequence 169032,
c	14	17	68.0	743	8	US-11-266-748A-250455	Sequence 250455,
c	15	17	68.0	743	8	US-11-266-748A-275004	Sequence 275004,
	16	17	68.0	743	8	US-11-266-748A-310972	Sequence 310972,
c	17	17	68.0	832	8	US-11-266-748A-169663	Sequence 169663,
	18	17	68.0	1475	8	US-11-266-748A-248983	Sequence 248983,
	19	17	68.0	1498	8	US-11-266-748A-352460	Sequence 352460,
c	20	17	68.0	1498	8	US-11-266-748A-435839	Sequence 435839,
	21	17	68.0	2020	9	US-11-218-305-16082	Sequence 16082, A
	22	17	68.0	3020	6	US-10-449-902-16511	Sequence 16511, A
	23	17	68.0	3421	6	US-10-449-902-15954	Sequence 15954, A
c	24	17	68.0	89567	6	US-10-539-228-838	Sequence 838, App
c	25	16.8	67.2	1000	8	US-11-266-748A-204578	Sequence 204578,
c	26	16.8	67.2	63411	6	US-10-540-898-57	Sequence 57, Appl
	27	16.8	67.2	183797	8	US-11-266-748A-22659	Sequence 22659, A
	28	16.6	66.4	415	8	US-11-266-748A-175427	Sequence 175427,
c	29	16.6	66.4	578	8	US-11-266-748A-16643	Sequence 16643, A
c	30	16.6	66.4	586	8	US-11-266-748A-380107	Sequence 380107,
	31	16.6	66.4	586	8	US-11-266-748A-463486	Sequence 463486,
c	32	16.6	66.4	753	8	US-11-266-748A-214105	Sequence 214105,
	33	16.6	66.4	761	8	US-11-266-748A-43177	Sequence 43177, A
	34	16.6	66.4	985	8	US-11-266-748A-181839	Sequence 181839,
c	35	16.6	66.4	985	8	US-11-266-748A-242366	Sequence 242366,
	36	16.6	66.4	1000	8	US-11-266-748A-392955	Sequence 392955,
c	37	16.6	66.4	1000	8	US-11-266-748A-483673	Sequence 483673,
c	38	16.6	66.4	1036	8	US-11-266-748A-2618	Sequence 2618, Ap
	39	16.6	66.4	1097	8	US-11-266-748A-73567	Sequence 73567, A
c	40	16.6	66.4	1097	8	US-11-266-748A-126378	Sequence 126378,
c	41	16.6	66.4	1433	6	US-10-449-902-25916	Sequence 25916, A
c	42	16.6	66.4	1482	8	US-11-266-748A-354069	Sequence 354069,
c	43	16.6	66.4	1482	8	US-11-266-748A-384757	Sequence 384757,
	44	16.6	66.4	1482	8	US-11-266-748A-437448	Sequence 437448,
c	45	16.6	66.4	3070	6	US-10-449-902-26992	Sequence 26992, A

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b-42.rst.

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2006, 16:33:29 ; Search time 213.308 Seconds
 (without alignments)
 6553.828 Million cell updates/sec

Title: US-09-995-225B-42
 Perfect score: 25
 Sequence: 1 gaggcagtagttgccacacctatgg 25

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	25	100.0	448	11	AQ225693	AQ225693 HS_2009_B
c	2	20.2	80.8	746	5	CD636851	CD636851 56003360H
c	3	19.4	77.6	445	4	CB413066	CB413066 ScaE_1551
	4	19	76.0	590	13	CL686359	CL686359 PRI0144a_
	5	19	76.0	808	13	CL692939	CL692939 PRI015b_F
	6	18.8	75.2	172	7	AW799209	AW799209 RC0-UM005
c	7	18.8	75.2	334	1	AI029980	AI029980 UI-R-C0-j
	8	18.8	75.2	565	5	CD636852	CD636852 56003360J
	9	18.8	75.2	634	9	DN376539	DN376539 LIB38529_
	10	18.8	75.2	697	3	BU616836	BU616836 UI-H-FH1-
	11	18.8	75.2	715	6	AB228360	AB228360 Aspergill
	12	18.8	75.2	729	8	CO138524	CO138524 EST833195
c	13	18.6	74.4	453	11	AZ009690	AZ009690 RPCI-23-3
c	14	18.6	74.4	483	2	BJ260234	BJ260234 BJ260234
c	15	18.6	74.4	489	2	BI680378	BI680378 458624 MA
c	16	18.6	74.4	495	2	BJ260587	BJ260587 BJ260587
c	17	18.6	74.4	499	10	DR463414	DR463414 CM118B10
c	18	18.6	74.4	504	4	BX499223	BX499223 DKFZp779E
c	19	18.6	74.4	506	7	AW653346	AW653346 101999 MA
c	20	18.6	74.4	543	1	AV591426	AV591426 AV591426
c	21	18.6	74.4	546	7	BF076557	BF076557 226150 MA
c	22	18.6	74.4	546	8	CO845205	CO845205 LM_GM5_00
c	23	18.6	74.4	557	2	BG691654	BG691654 340911 BA
c	24	18.6	74.4	572	2	BM030860	BM030860 495388 MA
c	25	18.6	74.4	590	2	BI682340	BI682340 463396 MA
c	26	18.6	74.4	590	7	BE590190	BE590190 197189 BA
	27	18.6	74.4	597	10	DT428100	DT428100 JGI_CABJ7
	28	18.6	74.4	613	1	AL781067	AL781067 AL781067
	29	18.6	74.4	619	1	AL802528	AL802528 AL802528
c	30	18.6	74.4	621	2	BJ260398	BJ260398 BJ260398
	31	18.6	74.4	639	1	AL656915	AL656915 AL656915
	32	18.6	74.4	640	1	AL876764	AL876764 AL876764
	33	18.6	74.4	642	1	AL877073	AL877073 AL877073
c	34	18.6	74.4	652	5	CK835565	CK835565 4059962 B
	35	18.6	74.4	661	1	AL629682	AL629682 AL629682
c	36	18.6	74.4	666	8	CO845204	CO845204 LM_GM5_00
c	37	18.6	74.4	668	14	CT344047	CT344047 Sus scrof
	38	18.6	74.4	677	8	CV037686	CV037686 4134688 B
c	39	18.6	74.4	708	5	CK951479	CK951479 4090992 B
c	40	18.6	74.4	745	5	CK832878	CK832878 4056654 B
	41	18.6	74.4	746	9	CX365721	CX365721 JGI_XZT26
c	42	18.6	74.4	759	10	DV572567	DV572567 0058P0045
c	43	18.6	74.4	759	10	DV572568	DV572568 0058P0045
c	44	18.6	74.4	774	3	BU228619	BU228619 603400106
	45	18.6	74.4	776	9	CX442974	CX442974 JGI_XZG86

ALIGNMENTS

RESULT 1
AQ225693
LOCUS

AQ225693

448 bp

DNA

linear

GSS 26-SEP-1998

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b- 16.rag.

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OM protein - protein search, using sw model

Run on: August 23, 2006, 19:10:59 ; Search time 195 Seconds
(without alignments)
827.679 Million cell updates/sec

Title: US-09-995-225B-16
Perfect score: 1872
Sequence: 1 MEHTHAHLAANSSLSWSPG.....CIKMLVYQYDKNGKPIKVSP 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1872	100.0	353	5	AAU76416	Aau76416 Novel G-p
2	1872	100.0	353	5	ABJ04075	Abj04075 Human G p
3	1872	100.0	353	5	ABB79517	Abb79517 Human che
4	1872	100.0	353	6	ABP98724	Abp98724 Human AXO
5	1872	100.0	353	6	ABR44437	Abr44437 Human G p
6	1872	100.0	353	6	ABB82499	Abb82499 Human TGR
7	1872	100.0	353	8	ADR16434	Adr16434 Human KOR
8	1872	100.0	591	7	ADF70485	Adf70485 Orphan re
9	1868	99.8	353	4	AAU10068	Aau10068 Chemokine
10	1868	99.8	353	7	ADJ87769	Adj87769 G-coupled
11	1868	99.8	353	8	ADI79325	Adi79325 NOV11 pro
12	1868	99.8	353	8	ADO56004	Ado56004 Human NOV
13	1868	99.8	353	8	ADO28954	Ado28954 Human nov
14	1857	99.2	372	4	AAU10067	Aau10067 Chemokine
15	1857	99.2	372	5	AAE18645	Aae18645 Human G-p
16	1857	99.2	372	6	ABR62521	Abr62521 Human G-p
17	1857	99.2	372	7	ADD18023	Add18023 Human G-p
18	1857	99.2	372	7	ADJ87767	Adj87767 G-coupled
19	1857	99.2	372	8	ADI79323	Adi79323 NOV10a pr
20	1852	98.9	372	8	ADO56002	Ado56002 Human NOV
21	1844	98.5	353	5	AAE29236	Aae29236 Human 7TM
22	1844	98.5	353	6	ABG71163	Abg71163 Novel hum
23	1844	98.5	353	6	ABU09571	Abu09571 Human pro
24	1841	98.3	369	6	ABR62522	Abr62522 Human G-p
25	1756	93.8	345	6	ABB82508	Abb82508 Mouse TGR
26	1756	93.8	345	8	ADO28956	Ado28956 Mouse nov
27	1643	87.8	318	7	ADJ87772	Adj87772 G-coupled
28	1643	87.8	318	8	ADI79348	Adi79348 NOV10b pr
29	1643	87.8	318	8	ADO56027	Ado56027 Human NOV
30	1638	87.5	333	5	AAE17081	Aae17081 Human G-p
31	1638	87.5	333	7	ABW00814	Abw00814 Human GPC
32	1638	87.5	343	5	ABB79519	Abb79519 Human che
33	1638	87.5	356	5	ABB79518	Abb79518 Human che
34	1638	87.5	385	5	ABP95606	Abp95606 Human GPC
35	1638	87.5	388	8	ADQ89946	Adq89946 Antagonis
36	1626	86.9	333	5	AAE17229	Aae17229 Human thy
37	1471	78.6	287	4	AAU25559	Aau25559 Human G P
38	1421	75.9	321	7	ADC12696	Adc12696 Human GPC
39	1317	70.4	265	6	ABP81706	Abp81706 Human G p
40	1317	70.4	265	6	ABR62524	Abr62524 Human G-p
41	912.5	48.7	313	4	AAU25556	Aau25556 Human G P
42	742	39.6	340	8	ADO28936	Ado28936 Mouse nov
43	742	39.6	348	6	ABR82431	Abr82431 Murine is
44	737	39.4	374	5	ABJ04070	Abj04070 Human G p
45	737	39.4	374	5	AAM49155	Aam49155 Human G p

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OM protein - protein search, using sw model

```
Run on:      August 23, 2006, 19:20:08 ; Search time 50 Seconds
              (without alignments)
              617.966 Million cell updates/sec
```

Title: US-09-995-225B-16
Perfect score: 1872
Sequence: 1 MEHTHAHLAANSSLSWSPG.....CIKMLVYQYDKNGKPIKVSP 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Issued_Patents_AA:*
1:   /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2:   /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3:   /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4:   /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5:   /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6:   /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7:   /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
--------	-------	------------------	--------	----	----	-------------

1	241	12.9	393	1	US-07-629-104I-3	Sequence 3, Appli
2	238.5	12.7	398	1	US-08-288-663A-1	Sequence 1, Appli
3	232	12.4	412	2	US-10-088-744A-8	Sequence 8, Appli
4	232	12.4	415	2	US-09-545-944-2	Sequence 2, Appli
5	232	12.4	415	2	US-10-215-619-2	Sequence 2, Appli
6	232	12.4	415	2	US-10-088-744A-6	Sequence 6, Appli
7	231.5	12.4	355	1	US-08-012-988A-2	Sequence 2, Appli
8	231.5	12.4	355	1	US-08-450-393A-5	Sequence 5, Appli
9	231.5	12.4	355	2	US-08-446-669-5	Sequence 5, Appli
10	231.5	12.4	355	2	US-09-239-938-1	Sequence 1, Appli
11	231.5	12.4	355	2	US-09-886-319A-14	Sequence 14, Appl
12	231.5	12.4	355	2	US-10-039-659A-13	Sequence 13, Appl
13	231.5	12.4	355	2	US-09-961-068-1	Sequence 1, Appli
14	231.5	12.4	355	2	US-09-625-573-5	Sequence 5, Appli
15	231.5	12.4	355	2	US-09-960-547-1	Sequence 1, Appli
16	231.5	12.4	355	5	PCT-US95-00476-5	Sequence 5, Appli
17	228	12.2	412	2	US-09-949-016-10101	Sequence 10101, A
18	228	12.2	412	2	US-10-088-744A-4	Sequence 4, Appli
19	228	12.2	415	2	US-09-875-076-12	Sequence 12, Appl
20	228	12.2	415	2	US-10-088-744A-2	Sequence 2, Appli
21	228	12.2	415	3	US-09-609-146-4	Sequence 4, Appli
22	226.5	12.1	398	1	US-08-288-663A-15	Sequence 15, Appl
23	226	12.1	415	2	US-09-341-016A-1	Sequence 1, Appli
24	225	12.0	357	2	US-09-693-746-4	Sequence 4, Appli
25	225	12.0	357	2	US-09-693-746-8	Sequence 8, Appli
26	223.5	11.9	355	2	US-08-833-752-9	Sequence 9, Appli
27	223.5	11.9	355	2	US-09-938-719-9	Sequence 9, Appli
28	223.5	11.9	355	2	US-09-939-226B-9	Sequence 9, Appli
29	223.5	11.9	355	2	US-09-938-703B-9	Sequence 9, Appli
30	223	11.9	352	2	US-09-029-027B-2	Sequence 2, Appli
31	222.5	11.9	347	1	US-08-118-270-47	Sequence 47, Appl
32	222.5	11.9	347	5	PCT-US93-08528-47	Sequence 47, Appl
33	219	11.7	353	1	US-08-118-270-45	Sequence 45, Appl
34	219	11.7	353	5	PCT-US93-08528-45	Sequence 45, Appl
35	219	11.7	367	1	US-08-149-093A-4	Sequence 4, Appli
36	219	11.7	367	1	US-08-911-245-4	Sequence 4, Appli
37	219	11.7	367	1	US-08-553-058C-4	Sequence 4, Appli
38	219	11.7	367	1	US-08-514-451A-4	Sequence 4, Appli
39	219	11.7	367	2	US-09-170-331-4	Sequence 4, Appli
40	219	11.7	367	2	US-09-510-473-4	Sequence 4, Appli
41	219	11.7	367	2	US-09-048-916B-4	Sequence 4, Appli
42	219	11.7	384	2	US-09-071-434-3	Sequence 3, Appli
43	218	11.6	378	2	US-09-045-583-5	Sequence 5, Appli
44	218	11.6	378	2	US-09-534-185-5	Sequence 5, Appli
45	217	11.6	355	2	US-09-045-583-53	Sequence 53, Appl

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b-16.rapbm.

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OM protein - protein search, using sw model

```
Run on:      August 23, 2006, 19:32:04 ; Search time 184 Seconds
              (without alignments)
              888.668 Million cell updates/sec
```

Title: US-09-995-225B-16
Perfect score: 1872
Sequence: 1 MEHTHAHLAANSSLSWSPG.....CIKMLVYQYDKNGKPIKVSP 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Published_Applications_AA_Main:*
1:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	%					
Result	Query					
No.	Score	Match Length DB	ID			Description

1	1872	100.0	353	3	US-09-995-225-16	Sequence 16, Appl
2	1872	100.0	353	3	US-09-995-225-16	Sequence 16, Appl
3	1872	100.0	353	4	US-10-094-417-2	Sequence 2, Appli
4	1872	100.0	353	4	US-10-296-294A-5	Sequence 5, Appli
5	1872	100.0	353	4	US-10-450-590-2	Sequence 2, Appli
6	1872	100.0	353	4	US-10-779-104-2	Sequence 2, Appli
7	1872	100.0	353	6	US-11-086-846-2	Sequence 2, Appli
8	1872	100.0	591	5	US-10-505-486-108	Sequence 108, App
9	1868	99.8	353	3	US-09-813-432-22	Sequence 22, Appl
10	1868	99.8	353	4	US-10-174-364-22	Sequence 22, Appl
11	1868	99.8	353	4	US-10-246-583-22	Sequence 22, Appl
12	1868	99.8	353	4	US-10-689-832-22	Sequence 22, Appl
13	1857	99.2	350	3	US-09-813-432-60	Sequence 60, Appl
14	1857	99.2	350	4	US-10-174-364-60	Sequence 60, Appl
15	1857	99.2	350	4	US-10-246-583-60	Sequence 60, Appl
16	1857	99.2	350	4	US-10-689-832-60	Sequence 60, Appl
17	1857	99.2	372	3	US-09-813-432-20	Sequence 20, Appl
18	1857	99.2	372	4	US-10-219-834-19	Sequence 19, Appl
19	1857	99.2	372	4	US-10-314-076-2	Sequence 2, Appli
20	1857	99.2	372	4	US-10-174-364-20	Sequence 20, Appl
21	1857	99.2	372	4	US-10-333-946-6	Sequence 6, Appli
22	1857	99.2	372	4	US-10-246-583-20	Sequence 20, Appl
23	1857	99.2	372	4	US-10-689-832-20	Sequence 20, Appl
24	1857	99.2	372	4	US-10-712-615-103	Sequence 103, App
25	1853	99.0	350	3	US-09-813-432-59	Sequence 59, Appl
26	1853	99.0	350	4	US-10-174-364-59	Sequence 59, Appl
27	1853	99.0	350	4	US-10-246-583-59	Sequence 59, Appl
28	1853	99.0	350	4	US-10-689-832-59	Sequence 59, Appl
29	1844	98.5	353	4	US-10-012-140-11	Sequence 11, Appl
30	1844	98.5	353	6	US-11-206-587-11	Sequence 11, Appl
31	1841	98.3	369	4	US-10-314-076-4	Sequence 4, Appli
32	1756	93.8	345	4	US-10-094-417-20	Sequence 20, Appl
33	1756	93.8	345	6	US-11-086-846-20	Sequence 20, Appl
34	1643	87.8	318	4	US-10-174-364-85	Sequence 85, Appl
35	1643	87.8	318	4	US-10-246-583-85	Sequence 85, Appl
36	1638	87.5	333	4	US-10-079-384-26	Sequence 26, Appl
37	1638	87.5	343	4	US-10-450-590-8	Sequence 8, Appli
38	1638	87.5	356	4	US-10-450-590-7	Sequence 7, Appli
39	1638	87.5	385	4	US-10-343-650A-22	Sequence 22, Appl
40	1638	87.5	388	5	US-10-745-237-376	Sequence 376, App
41	1626	86.9	333	5	US-10-297-990A-2	Sequence 2, Appli
42	1471	78.6	287	3	US-09-791-932-66	Sequence 66, Appl
43	1471	78.6	287	5	US-10-980-388-66	Sequence 66, Appl
44	1426	76.2	272	3	US-09-813-432-57	Sequence 57, Appl
45	1426	76.2	272	3	US-09-813-432-58	Sequence 58, Appl

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b-16.rapbn.

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OM protein - protein search, using sw model

```
Run on:      August 23, 2006, 19:32:44 ; Search time 34 Seconds
              (without alignments)
              703.448 Million cell updates/sec
```

Title: US-09-995-225B-16
Perfect score: 1872
Sequence: 1 MEHTHAHLAANSSLSWSPG.....CIKMLVYQYDKNGKPIKVSP 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 243793 seqs, 67754213 residues

Total number of hits satisfying chosen parameters: 243793

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      Published_Applications_AA_New:*
1:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	$\frac{8}{10}$ Query
--------	-------------------------

No.	Score	Match Length	DB	ID	Description	
1	213	11.4	352	6	US-10-505-928-745	Sequence 745, App
2	213	11.4	352	6	US-10-511-937-2486	Sequence 2486, Ap
3	213	11.4	352	6	US-10-511-937-2935	Sequence 2935, Ap
4	213	11.4	352	6	US-10-511-937-3010	Sequence 3010, Ap
5	211.5	11.3	380	7	US-11-302-678-20	Sequence 20, Appl
6	207.5	11.1	428	7	US-11-053-553-3	Sequence 3, Appli
7	206.5	11.0	317	6	US-10-539-228-163	Sequence 163, App
8	205	11.0	355	7	US-11-389-101-2	Sequence 2, Appli
9	204.5	10.9	355	7	US-11-367-538-2	Sequence 2, Appli
10	204	10.9	355	7	US-11-133-140-6	Sequence 6, Appli
11	204	10.9	372	7	US-11-271-383-4	Sequence 4, Appli
12	201.5	10.8	423	7	US-11-285-580-2	Sequence 2, Appli
13	199.5	10.7	352	6	US-10-511-937-2412	Sequence 2412, Ap
14	199.5	10.7	352	6	US-10-994-679-22	Sequence 22, Appl
15	199.5	10.7	372	7	US-11-271-383-2	Sequence 2, Appli
16	198	10.6	403	7	US-11-242-505A-18	Sequence 18, Appl
17	193.5	10.3	352	6	US-10-994-679-2	Sequence 2, Appli
18	191.5	10.2	356	7	US-11-384-847-7	Sequence 7, Appli
19	190.5	10.2	346	7	US-11-376-694-1	Sequence 1, Appli
20	190	10.1	348	6	US-10-540-898-921	Sequence 921, App
21	189	10.1	380	6	US-10-540-898-443	Sequence 443, App
22	188	10.0	370	7	US-11-376-694-3	Sequence 3, Appli
23	186.5	10.0	392	6	US-10-504-973-8	Sequence 8, Appli
24	184.5	9.9	364	7	US-11-255-699-1	Sequence 1, Appli
25	182	9.7	389	6	US-10-565-487-1	Sequence 1, Appli
26	180.5	9.6	347	7	US-11-389-101-3	Sequence 3, Appli
27	180.5	9.6	424	7	US-11-242-505A-33	Sequence 33, Appl
28	180.5	9.6	424	7	US-11-255-699-3	Sequence 3, Appli
29	177.5	9.5	366	7	US-11-255-699-2	Sequence 2, Appli
30	177	9.5	465	7	US-11-255-699-4	Sequence 4, Appli
31	176	9.4	259	7	US-11-283-567-3	Sequence 3, Appli
32	174.5	9.3	344	6	US-10-994-679-9	Sequence 9, Appli
33	173.5	9.3	365	7	US-11-360-239-2	Sequence 2, Appli
34	170.5	9.1	355	6	US-10-540-898-918	Sequence 918, App
35	170	9.1	332	7	US-11-257-851A-77	Sequence 77, Appl
36	169	9.0	378	6	US-10-511-937-2404	Sequence 2404, Ap
37	169	9.0	423	7	US-11-312-958-12	Sequence 12, Appl
38	168	9.0	332	7	US-11-289-102-247	Sequence 247, App
39	168	9.0	354	6	US-10-516-032-12	Sequence 12, Appl
40	166	8.9	296	7	US-11-400-159-2	Sequence 2, Appli
41	166	8.9	423	7	US-11-336-098-2	Sequence 2, Appli
42	165	8.8	368	6	US-10-511-937-2505	Sequence 2505, Ap
43	165	8.8	368	6	US-10-511-937-2931	Sequence 2931, Ap
44	165	8.8	368	7	US-11-302-678-59	Sequence 59, Appl
45	164.5	8.8	297	7	US-11-257-851A-73	Sequence 73, Appl

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OM protein - protein search, using sw model

```
Run on:      August 23, 2006, 19:15:03 ; Search time 41 Seconds
              (without alignments)
              828.403 Million cell updates/sec
```

Title: US-09-995-225B-16
Perfect score: 1872
Sequence: 1 MEHTHAHLAANSSLSWSPG.....CIKMLVYQYDKNGKPIKVSP 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      PIR_80:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description
		% Match	Length	DB		
1	242	12.9	411	2	I56444	thyrotrophin-relea
2	242	12.9	412	2	S23436	thyroliberin rece

3	241	12.9	393	2	A39251	thyrotropin-releas
4	238.5	12.7	398	2	JN0708	thyrotropin-releas
5	231.5	12.4	355	2	A45177	chemokine (C-C) re
6	226	12.1	352	2	JE0296	thyrotropin releas
7	225	12.0	357	2	JC7319	probable allatosta
8	219.5	11.7	388	2	JN0605	somatostatin recep
9	219	11.7	384	2	A47249	brain-specific som
10	218	11.6	423	2	JC7677	allatostatin recep
11	217.5	11.6	340	2	T18704	hypothetical prote
12	217.5	11.6	394	2	JC7209	galanin receptor -
13	217.5	11.6	658	2	JC8011	G protein-coupled
14	217	11.6	367	2	JC2421	opioid receptor ho
15	217	11.6	367	2	I49022	kappa opioid recep
16	217	11.6	367	2	I56520	G protein-coupled
17	214.5	11.5	595	2	JC8012	G protein-coupled
18	213.5	11.4	355	2	I49339	macrophage inflamm
19	213	11.4	352	2	A45747	neuropeptide Y/pep
20	213	11.4	370	2	S43087	orphan opioid rece
21	213	11.4	384	2	JC4629	somatostatin recep
22	212	11.3	360	2	T23063	hypothetical prote
23	211.5	11.3	376	2	T24368	hypothetical prote
24	211.5	11.3	380	2	JC2338	kappa opioid recep
25	211.5	11.3	504	2	T29338	hypothetical prote
26	210.5	11.2	380	2	S36143	kappa opioid recep
27	209	11.2	424	2	JH0164	neurotensin recept
28	208.5	11.1	363	2	I57940	somatostatin recep
29	207.5	11.1	399	2	A46632	bombesin-like pept
30	207.5	11.1	428	2	JN0692	cholecystokinin ty
31	206.5	11.0	380	2	A48227	kappa opioid recep
32	206.5	11.0	380	2	JC2434	kappa opioid recep
33	206.5	11.0	391	2	A41795	somatostatin recep
34	206.5	11.0	391	2	C41795	somatostatin recep
35	205.5	11.0	353	2	JC2492	G protein-coupled
36	205.5	11.0	391	2	A39297	somatostatin recep
37	205	11.0	355	2	G02436	chemokine (C-C) re
38	205	11.0	355	2	JC5067	G protein-coupled
39	205	11.0	418	2	S59601	vasopressin recept
40	204.5	10.9	352	2	S60024	bradykinin B1 rece
41	204.5	10.9	380	2	A55259	kappa opioid recep
42	204	10.9	353	2	S28787	neuropeptide Y/pep
43	204	10.9	372	2	I38532	delta opioid recep
44	203.5	10.9	314	2	T15831	hypothetical prote
45	203.5	10.9	477	2	JC7913	capa receptor (CG1

SCORE Search Results Details for Application 09995225 and Search Result us-09-995-225b-16.rup.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
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OM protein - protein search, using sw model

Run on: August 23, 2006, 19:11:33 ; Search time 301 Seconds
(without alignments)
1084.819 Million cell updates/sec

Title: US-09-995-225B-16
Perfect score: 1872
Sequence: 1 MEHTHAHLAANSSLSWSPG.....CIKMLVYQYDKNGKPIKVSP 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :      UniProt_7.2:*
1:  uniprot_sprot:*
2:  uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARY							
Result	%		Query				
No.	Score	Match	Length	DB	ID	Description	
1	1872	100.0	353	1	GP139_HUMAN	Q6dwj6 homo sapien	
2	1757	93.9	345	1	GP139_RAT	P0c0w8 rattus norv	
3	1756	93.8	345	1	GP139_MOUSE	Q80uc8 mus musculu	
4	1752	93.6	345	2	Q2VY20_MOUSE	Q2vy20 mus musculu	

5	1317	70.4	265	2	Q9BYT4_HUMAN	Q9byt4	homo sapien
6	1277.5	68.2	383	2	Q7T2L1_FUGRU	Q7t2l1	fugu rubrip
7	1175	62.8	327	2	Q4RJM0_TETNG	Q4rjm0	tetraodon n
8	782	41.8	309	2	Q4S8I3_TETNG	Q4s8i3	tetraodon n
9	771	41.2	371	2	Q7T2L2_FUGRU	Q7t2l2	fugu rubrip
10	737	39.4	462	1	GP142_HUMAN	Q7z601	homo sapien
11	737	39.4	1464	2	Q8NGB0_HUMAN	Q8ngb0	homo sapien
12	713	38.1	365	1	GP142_MOUSE	Q7tqn9	mus musculu
13	263.5	14.1	358	2	Q4RJX3_TETNG	Q4rjx3	tetraodon n
14	262.5	14.0	374	2	Q5FB96_BOMMO	Q5fb96	bombyx mori
15	260.5	13.9	394	2	Q17478_CAEEL	Q17478	caenorhabdi
16	250.5	13.4	398	1	TRFR_BOVIN	O46639	bos taurus
17	249.5	13.3	398	1	TRFR_SHEEP	Q28596	ovis aries
18	249.5	13.3	440	2	Q7PYB7_ANOGA	Q7pyb7	anopheles g
19	248	13.2	549	1	FMAR_DROME	Q9vzw5	drosophila
20	242	12.9	412	1	TRFR_RAT	Q01717	rattus norv
21	241	12.9	393	1	TRFR_MOUSE	P21761	mus musculu
22	241	12.9	393	2	Q32MS1_MOUSE	Q32ms1	mus musculu
23	241	12.9	478	2	Q2LYS7_DROPS	Q2lys7	drosophila
24	240.5	12.8	413	2	Q65YS4_BOMMO	Q65ys4	bombyx mori
25	239	12.8	393	2	Q3UYL6_MOUSE	Q3uyl6	mus musculu
26	238.5	12.7	398	1	TRFR_HUMAN	P34981	homo sapien
27	238.5	12.7	398	2	Q2M339_HUMAN	Q2m339	homo sapien
28	238	12.7	394	2	Q620B8_CAEER	Q620b8	caenorhabdi
29	236	12.6	488	2	Q717R7_DROME	Q717r7	drosophila
30	235.5	12.6	395	1	TRFR_CHICK	O93603	gallus gall
31	235	12.6	354	2	Q2V0Q7_CANFA	Q2v0q7	canis famil
32	235	12.6	404	2	Q8JFZ7_XENLA	Q8j fz7	xenopus lae
33	234	12.5	478	2	Q717T5_DROME	Q717t5	drosophila
34	233.5	12.5	354	2	Q6YST0_PIG	Q6yst0	sus scrofa
35	233	12.4	397	2	Q9DDR1_XENLA	Q9ddr1	xenopus lae
36	233	12.4	478	2	Q9W025_DROME	Q9w025	drosophila
37	232	12.4	435	2	Q8SWR3_DROME	Q8swr3	drosophila
38	231.5	12.4	355	1	CCR1_HUMAN	P32246	homo sapien
39	231.5	12.4	355	2	Q5U003_HUMAN	Q5u003	homo sapien
40	231.5	12.4	355	2	Q9MYJ8_CALJA	Q9myj8	callithrix
41	231	12.3	397	2	Q8JFZ5_XENLA	Q8j fz5	xenopus lae
42	230.5	12.3	381	2	Q7PHG9_ANOGA	Q7phg9	anopheles g
43	230.5	12.3	427	2	Q330M5_ANOGA	Q330m5	anopheles g
44	230.5	12.3	427	2	Q7RTK2_ANOGA	Q7rtk2	anopheles g
45	230.5	12.3	547	2	Q2LYS6_DROPS	Q2lys6	drosophila